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SEQUENCE LISTING

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Young, N. Martin  
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National Research Council of Canada

<120> Fusion Proteins for Use in Enzymatic Synthesis of  
Oligosaccharides

<130> 019957-012910US

<140> US 09/211,691

<141> 1998-12-14

<150> US 60/069,443

<151> 1997-12-15

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 828

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(828)

<223> beta-1,4-galactosyltransferase (lgtB)

<400> 1

atg caa aac cac gtt atc agc tta gct tcc gcc gca gaa cgc agg gcg 48  
Met Gln Asn His Val Ile Ser Leu Ala Ser Ala Ala Glu Arg Arg Ala  
1 5 10 15

cac att gcc gat acc ttc ggc agg cac ggc atc ccg ttt cag ttt ttc 96  
His Ile Ala Asp Thr Phe Gly Arg His Gly Ile Pro Phe Gln Phe Phe  
20 25 30

gac gca ctg atg ccg tct gaa agg ctg gaa cag gca atg gcg gaa ctc 144  
Asp Ala Leu Met Pro Ser Glu Arg Leu Glu Gln Ala Met Ala Glu Leu  
35 40 45

gtc ccc ggc ttg tcg gcg cac ccc tat ttg agc gga gtg gaa aaa gcc 192  
Val Pro Gly Leu Ser Ala His Pro Tyr Leu Ser Gly Val Glu Lys Ala  
50 55 60

tgc ttt atg agc cac gcc gta ttg tgg aag cag gca ttg gac gaa ggt 240  
Cys Phe Met Ser His Ala Val Leu Trp Lys Gln Ala Leu Asp Glu Gly  
65 70 75 80

ctg ccg tat atc acc gta ttt gag gac gac gtt tta ctc ggc gaa ggt 288  
Leu Pro Tyr Ile Thr Val Phe Glu Asp Asp Val Leu Leu Gly Glu Gly  
85 90 95

gag gaa aaa ttc ctt gcc gaa gac gct tgg ctg caa gaa cgc ttt gac 336  
Glu Glu Lys Phe Leu Ala Glu Asp Ala Trp Leu Gln Glu Arg Phe Asp  
100 105 110

a2

✓

ccg gat acc gcc ttt atc gtc cgc ttg gaa acg atg ttt atg cac gtc 384  
 Pro Asp Thr Ala Phe Ile Val Arg Leu Glu Thr Met Phe Met His Val  
 115 120 125

ctg acc tgc ccc tcc ggc gtg gcg gat tac tgc ggg cgc gcc ttt ccg 432  
 Leu Thr Ser Pro Ser Gly Val Ala Asp Tyr Cys Gly Arg Ala Phe Pro  
 130 135 140

ctg ttg gaa agc gaa cac tgg ggg acg gcg ggc tat atc att tcc cga 480  
 Leu Leu Glu Ser Glu His Trp Gly Thr Ala Gly Tyr Ile Ile Ser Arg  
 145 150 155 160

aaa gcg atg cgg ttt ttc ctg gac agg ttt gcc gcc ctg ccg ccc gaa 528  
 Lys Ala Met Arg Phe Phe Leu Asp Arg Phe Ala Ala Leu Pro Pro Glu  
 165 170 175

ggg ctg cac ccc gtc gat ctg atg atg ttc agc gat ttt ttc gac agg 576  
 Gly Leu His Pro Val Asp Leu Met Met Phe Ser Asp Phe Phe Asp Arg  
 180 185 190

gaa gga atg ccg gtt tgc cag ctc aat ccc gcc ttg tgc gcc caa gag 624  
 Glu Gly Met Pro Val Cys Gln Leu Asn Pro Ala Leu Cys Ala Gln Glu  
 195 200 205

ctg cat tat gcc aag ttt cac gac caa aac agc gca ttg ggc agc ctg 672  
 Leu His Tyr Ala Lys Phe His Asp Gln Asn Ser Ala Leu Gly Ser Leu  
 210 215 220

atc gaa cac gac cgc ctc ctg aac cgc aaa cag caa agg cgc gat tcc 720  
 Ile Glu His Asp Arg Leu Leu Asn Arg Lys Gln Gln Arg Arg Asp Ser  
 225 230 235 240

ccc gcc aac aca ttc aaa cac cgc ctg atc cgc gcc ttg acc aaa atc 768  
 Pro Ala Asn Thr Phe Lys His Arg Leu Ile Arg Ala Leu Thr Lys Ile  
 245 250 255

agc agg gaa agg gaa aaa cgc cgg caa agg cgc gaa cag ttc att gtg 816  
 Ser Arg Glu Arg Glu Lys Arg Arg Gln Arg Arg Glu Gln Phe Ile Val  
 260 265 270

cct ttc caa taa 828  
 Pro Phe Gln  
 275

a2  
 cont

<210> 2  
 <211> 275  
 <212> PRT  
 <213> Neisseria meningitidis

<400> 2  
 Met Gln Asn His Val Ile Ser Leu Ala Ser Ala Ala Glu Arg Arg Ala  
 1 5 10 15  
 His Ile Ala Asp Thr Phe Gly Arg His Gly Ile Pro Phe Gln Phe Phe  
 20 25 30  
 Asp Ala Leu Met Pro Ser Glu Arg Leu Glu Gln Ala Met Ala Glu Leu  
 35 40 45  
 Val Pro Gly Leu Ser Ala His Pro Tyr Leu Ser Gly Val Glu Lys Ala  
 50 55 60  
 Cys Phe Met Ser His Ala Val Leu Trp Lys Gln Ala Leu Asp Glu Gly  
 65 70 75 80

Leu Pro Tyr Ile Thr Val Phe Glu Asp Asp Val Leu Leu Gly Glu Gly  
                     85                    90                    95  
 Glu Glu Lys Phe Leu Ala Glu Asp Ala Trp Leu Gln Glu Arg Phe Asp  
                     100                    105                    110  
 Pro Asp Thr Ala Phe Ile Val Arg Leu Glu Thr Met Phe Met His Val  
                     115                    120                    125  
 Leu Thr Ser Pro Ser Gly Val Ala Asp Tyr Cys Gly Arg Ala Phe Pro  
                     130                    135                    140  
 Leu Leu Glu Ser Glu His Trp Gly Thr Ala Gly Tyr Ile Ile Ser Arg  
                     145                    150                    155                    160  
 Lys Ala Met Arg Phe Phe Leu Asp Arg Phe Ala Ala Leu Pro Pro Glu  
                     165                    170                    175  
 Gly Leu His Pro Val Asp Leu Met Met Phe Ser Asp Phe Phe Asp Arg  
                     180                    185                    190  
 Glu Gly Met Pro Val Cys Gln Leu Asn Pro Ala Leu Cys Ala Gln Glu  
                     195                    200                    205  
 Leu His Tyr Ala Lys Phe His Asp Gln Asn Ser Ala Leu Gly Ser Leu  
                     210                    215                    220  
 Ile Glu His Asp Arg Leu Leu Asn Arg Lys Gln Gln Arg Arg Asp Ser  
                     225                    230                    235                    240  
 Pro Ala Asn Thr Phe Lys His Arg Leu Ile Arg Ala Leu Thr Lys Ile  
                     245                    250                    255  
 Ser Arg Glu Arg Glu Lys Arg Arg Gln Arg Arg Glu Gln Phe Ile Val  
                     260                    265                    270  
 Pro Phe Gln  
                     275

<210> 3  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:SYNTM-F1 5'  
 primer

<400> 3  
 cttaggaggt catatggaaa aacaaaatat tgcgggtata c

41

<210> 4  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:SYNTM-R6 3'  
 primer

<400> 4  
 cgacagaatt ccgccaccgc tttccttgatg attaagaatg ttttc

45

<210> 5  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

a2  
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<220>

<223> Description of Artificial Sequence:SIALM-22F 5'  
primer

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gcatggaatt ctgggcttga aaaaggcttg ttgacc

37

<210> 6

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SIALM-23R 3'  
primer

<400> 6

cctaggtoga ctcattagt gtgatggtgg tgatggttca ggtcttcttc gctgatcag 59

<210> 7

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:linker of  
pFUS-01/2

<400> 7

Gly Gly Gly Ile Leu Ser His Gly Ile

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5

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:linker of  
pFUS-01/4

<400> 8

Gly Gly Gly Ile Leu Ser Gly Ile

1

5

<210> 9

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:GalE-5p 5'  
primer

<400> 9

gggacaggat ccacgatgc ttaggagggtc atatggcaat ttagtatta ggtggagc 58

a2  
cont

<210> 10  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:GalE-3p 3'  
 primer

<400> 10  
 ggggggggcta gcgccgcctc ctcgatcatc gtaccctttt gg 42

<210> 11  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:LgtB-NheI 5'  
 primer

<400> 11  
 ggggggggcta gcgtgcaaaa ccacgttatc agcttagc 38

<210> 12  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:LgtB-SalI 3'  
 primer

<400> 12  
 ggggggggtcg acctattatt ggaaaggcac aatgaactgt tcgcg 45

<210> 13  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:peptide linker

<400> 13  
 Gly Gly Gly Ile Leu Ser His Gly Ile Leu  
 1 5 10

<210> 14  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:6-His tail for  
 purification

A2  
 cont.

<400> 14  
His His His His His His  
1 5

<210> 15  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:peptide linker

<400> 15  
Gly Gly Ala Ser Val  
1 5

<210> 16  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:junction region  
of the galE-lgtB fusion

<220>  
<221> CDS  
<222> (1)..(63)  
<223> junction region of the galE-lgtB fusion

<400> 16  
cca aaa ggg tac gat gat cga gga ggc gga gct agc gtg caa aac cac 48  
Pro Lys Gly Tyr Asp Asp Arg Gly Gly Gly Ala Ser Val Gln Asn His  
1 5 10 15

gtt atc agc tta gct 63  
Val Ile Ser Leu Ala  
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<210> 17  
<211> 21  
<212> PRT  
<213> Artificial Sequence  
<223> Description of Artificial Sequence:junction region  
of the galE-lgtB fusion

<400> 17  
Pro Lys Gly Tyr Asp Asp Arg Gly Gly Gly Ala Ser Val Gln Asn His  
1 5 10 15  
Val Ile Ser Leu Ala  
20

<210> 18  
<211> 4  
<212> PRT  
<213> Artificial Sequence

a2  
Cont

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:peptide linker

&lt;400&gt; 18

Gly Gly Gly Ile

1

a<sup>2</sup>  
cont